AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Please replace the paragraph at page 4, lines 11-21, with the following:

Figures 1A-1C show ~~Figure 1 shows~~ a comparison of the amino acid sequences of the 1-deoxy-D-xylulose 5-phosphate reductoisomerase from corn clone p0004.cb1hh74r (SEQ ID NO:16), rice clone rlr6.pk0073.d5 (SEQ ID NO:6), a soybean contig assembled from clones sml1c.pk001.c15, sml1c.pk005.a24, sl1.pk0021.a6, sl2.pk124.p17, sl1.pk0036.a5, sl2.pk0111.c9, sl1.pk152.i19, and sl2.pk0039.d4 (SEQ ID NO:8), a soybean contig assembled from clones ses2w.pk0029.e5, sgc3c.pk001.d16, and sr1.pk0008.d1:fis (SEQ ID NO:18), wheat clone wlm12.pk0003.d11:fis (SEQ ID NO:20), *Arabidopsis thaliana* (NCBI General Identifier No. 4886307; SEQ ID NO:21), and *Mentha x piperita* (NCBI General Identifier No. 4581856; SEQ ID NO:22). Amino acids conserved among all sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize alignment of the sequences.

Please replace the paragraph beginning at page 8, line 34, and continuing through page 9, line 18, with the following:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410~~; see also www.ncbi.nlm.nih.gov/BLAST/~~). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short

oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Please replace the paragraph at page 20, lines 17-33, with the following:

cDNA clones encoding isopentenyl diphosphate biosynthetic enzymes were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410~~; see also www.ncbi.nlm.nih.gov/BLAST/~~) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

Please replace the paragraph at page 22, lines 8-13, with the following:

Figures 1A-1C present ~~Figure 1 presents~~ an alignment of the amino acid sequences set forth in SEQ ID NOs:6, 8, 16, 18, and 20 and the *Arabidopsis thaliana* and *Mentha x piperita* sequences (SEQ ID NO:21 and SEQ ID NO:22). The data in Table 5 ~~Table 4~~ represents a calculation of the percent Identity of the amino acid sequences set forth in SEQ ID NOs:6, 8, 16, 18, and 20 and the *Arabidopsis thaliana* and *Mentha x piperita* sequences (SEQ ID NO:21 and SEQ ID NO:22).

Please replace Table 4, beginning at page 22, line 15, with the following:

TABLE 5 ~~TABLE 4~~

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to 1-Deoxy-D-Xylulose 5-Phosphate Reductoisomerase

SEQ ID NO.	Percent Identity to 4886307	Percent Identity to 4581856
16 ~~6~~	90.9	73.8
6 ~~8~~	91.6	73.0
18 ~~16~~	88.4	74.1
8 ~~18~~	77.6	66.1
20	89.7	72.2

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-24. (canceled)

25. (new) An isolated polynucleotide comprising:

(a) a nucleotide sequence encoding a polypeptide having 1-deoxy-D-xylulose 5-phosphate reductoisomerase activity, wherein the polypeptide has an amino acid sequence of at least 93% sequence identity, based on the Clustal V method of alignment, using pairwise alignment default parameters of KTUPLE=1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5, when compared to SEQ ID NO:8, or

(b) a complement of the nucleotide sequence of (a).

26. (new) The polynucleotide of Claim 25, wherein the amino acid sequence of the polypeptide has at least 95% sequence identity, based on the Clustal V method of alignment, using the pairwise alignment default parameters, when compared to SEQ ID NO:8.

27. (new) The polynucleotide of Claim 25, wherein the amino acid sequence of the polypeptide has at least 98% sequence identity, based on the Clustal V method of alignment, using the pairwise alignment default parameters, when compared to SEQ ID NO:8.

28. (new) The polynucleotide of Claim 25, wherein the amino acid sequence of the polypeptide comprises SEQ ID NO:8.

29. (new) The polynucleotide of Claim 25 wherein the nucleotide sequence comprises SEQ ID NO:7.

30. (new) A vector comprising the polynucleotide of Claim 25.

31. (new) A recombinant DNA construct comprising the polynucleotide of Claim 25 operably linked to at least one regulatory sequence.

32. (new) A method for transforming a cell, comprising transforming a cell with the polynucleotide of Claim 25.

33. (new) A cell comprising the recombinant DNA construct of Claim 31.

34. (new) A method for producing a transgenic plant comprising transforming a plant cell with the polynucleotide of Claim 25 and regenerating a transgenic plant from the transformed plant cell.

35. (new) A plant comprising the recombinant DNA construct of Claim 31.

36. (new) A seed comprising the recombinant DNA construct of Claim 31.

37. (new) A method for positive selection of a transformed cell comprising:

(a) transforming a host cell with the recombinant DNA construct of Claim 31; and

(b) growing the transformed host cell under conditions suitable for the expression of the polynucleotide in an amount sufficient to complement a 1-deoxy-D-xylulose 5-phosphate reductoisomerase mutant to provide a positive selection means.